## **Supporting Information**

## Increased number of teeth predict acquisition of mutans streptococci in infants

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## Appendix S1: Technical details of Structural equation modeling

A (generalized) SEM model incorporating both measurement (confirmatory factor analysis) and path models was used to fit the data. The mean structure of this model is as follows:

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logit[P(\text{birth grp} = 1)] = \beta_{10} + \beta_{11} Demographics

log[E(\text{numteeth }_{j})] = \beta_{20j} + \beta_{21j} FBiol + \beta_{12j} Demographics, _{j}=1, 2

logit[P(\text{hypo} = 1)] = \beta_{30} + \beta_{31} FBiol + \beta_{32} Demographics

logit[P(\text{FBehavmeas }_{j}=1)] = \beta_{40j} + \beta_{41j} FBehav + \beta_{42j} Demographics

E(\text{FBiol}) = \beta_{50} + \beta_{51} birth grp + \beta_{52} Demographics

E(\text{FBehav}) = \beta_{60} + \beta_{61} birth grp + \beta_{62} Demographics

logit[P(\text{MScaregiver} > k)] = \beta_{70k} + \beta_{71} Demographics, _{k}=0,1,2

logit[P(\text{MSinfant} = 1)] = \beta_{80} + \beta_{81} birth grp + \beta_{82} FBiol + \beta_{83} FBehav + \beta_{84} MScaregiver + \beta_{85} Demographics
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where logit (p) = log(p/1-p), hypo refers to presence of hypoplasia at 18-20 mos., FBehavmeas<sub>j</sub> is the *j*th measurement for FBehav (brush, snack, brstfeed, and dentaccess), and **Demographics** is a vector of demographic variables (caregiver race, education, age, and marital status) with corresponding (bolded) coefficient. Response variables are assumed to be independent, conditional on explanatory variables in the models. We assumed the latent response variables (FBiol, FBehav) to be normally distributed; birth grp (0=VLBW, 1=NBW), hypoplasia18-20 (0=no, 1=yes), brush (0=no, 1=yes), snack (0=no, 1=yes), brstfeed (0=no, 1=yes), dentaccess (0=no, 1=yes) , and MSinfant (0=no, 1=yes) are assumed Bernoulli; MScaregiver (with levels 0,...,3) is assumed multinomial; and number of teeth at 8 and 18-20 (numteeth<sub>1</sub>, numteeth<sub>2</sub>, respectively) are assumed negative binomial.